Claims

1. A method for distinguishing prognostically definable AML subtypes with normal karyotype into different prognosis subsets in a sample, the method comprising determining the expression level of markers selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Table 1,

wherein

a high expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 42, 43, 44, 46, 47, 48, 49, and/or 50 of Table 1,

is indicative for median event-free survival (EFS).

2. The method according to claim 1 wherein the polynucleotide is labelled.

3. The method according to claim 1 or 2, wherein the label is a luminescent, preferably a fluorescent label, an enzymatic or a radioactive label.

4. The method according at least one of the claims 1-3, wherein the expression level of at least two, preferably of at least ten, more preferably of at least 25, most preferably of 50 of the markers of at least one of the Table 1 is determined.

5. The method according to at least one of the claims 1-4, wherein the expression level of markers expressed lower in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold lower, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold lower in the first subtype.

6. The method according to at least one of the claims 1-4, wherein the expression level of markers expressed higher in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold higher, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold higher in the first subtype.

7. The method according to at least one of the claims 1-6, wherein the sample is from an individual having AML.

8. The method according to at least one of the claims 1-7, wherein at least one polynucleotide is in the form of a transcribed polynucleotide, or a portion thereof.

9. The method according to claim 8, wherein the transcribed polynucleotide is a mRNA or a cDNA.

10. The method according to claim 8 or 9, wherein the determining of the expression level comprises hybridizing the transcribed polynucleotide to a complementary polynucleotide, or a portion thereof, under stringent hybridization conditions.

11. The method according to at least one of the claims 1-7, wherein at least one polynucleotide is in the form of a polypeptide, or a portion thereof.

12. The method according to at least one of claims 8, 9 or 12, wherein the determining of the expression level comprises contacting the polynucleotide or the polypeptide with a compound specifically binding to the polynucleotide or the polypeptide.

13. The method according to claim 12, wherein the compound is an antibody, or a fragment thereof.

14. The method according to at least one of the claims 1-13, wherein the method is carried out on an array.

15. The method according to at least one of the claims 1-14, wherein the method is carried out in a robotics system.

16. The method according to at least one of the claims 1-15, wherein the method is carried out using microfluidics.

17. Use of at least one marker as defined in at least one of the claims 1-3 for the manufacturing of a diagnostic for distinguishing prognostically definable AML subtypes with normal karyotype.

18. The use according to claim 17 for distinguishing prognostically definable AML subtypes with normal karyotype into different prognosis subsets in an individual having AML.

19. A diagnostic kit containing at least one marker as defined in at least one of the claims 1-3 for distinguishing prognostically definable AML subtypes with normal karyotype, in combination with suitable auxiliaries.

20. The diagnostic kit according to claim 19, wherein the kit contains a reference for the prognostically definable AML subtypes with normal karyotype.

21. The diagnostic kit according to claim 20, wherein the reference is a sample or a data bank.

22. An apparatus for distinguishing prognostically definable AML subtypes with normal karyotype into different prognosis subsets in a sample containing a reference data bank.

23. The apparatus according to claim 22, wherein the reference data bank is obtainable by comprising

(a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Table 1, and

(b) classifying the gene expression profile by means of a machine learning algorithm.

24. The apparatus according to claim 23, wherein the machine learning algorithm is selected from the group consisting of Weighted Voting, K-Nearest Neighbors, Decision Tree Induction, Support Vector Machines, and Feed-Forward Neural Networks, preferably Support Vector Machines.

25. The apparatus according to at least one of the claims 22-24, wherein the apparatus contains a control panel and/or a monitor.

26. A reference data bank for distinguishing prognostically definable AML subtypes with normal karyotype into different prognosis subsetsobtainable by comprising

(a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Table 1 and

(b) classifying the gene expression profile by means of a machine learning algorithm.

27. The reference data bank according to claim 26, wherein the reference data bank is backed up and/or contained in a computational memory chip.